AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph starting on line 1 of page 49 as follows:

14-3-3 Family (14_3_3; Pfam Pfam Accession No. PF00244). SEQ ID NO:1053 corresponds to a sequence encoding a 14-3-3 protein family member. The 14-3-3 protein family includes a group of closely related acidic homodimeric proteins of about 30 kD first identified as very abundant in mammalian brain tissues and located preferentially in neurons (Aitken et al. *Trends Biochem. Sci.* (1995) *20*:95-97; Morrison *Science* (1994) *266*:56-57; and Xiao et al. *Nature* (1995) *376*:188-191). The 14-3-3 proteins have multiple biological activities, including a key role in signal transduction pathways and the cell cycle. 14-3-3 proteins interact with kinases (*e.g.*, PKC or Raf-1), and can also function as protein-kinase dependent activators of tyrosine and tryptophan hydroxylases. The 14-3-3 protein sequences are extremely well conserved, and include two highly conserved regions: the first is a peptide of 11 residues located in the N-terminal section; the second, a 20 amino acid region located in the C-terminal section. ~~The consensus patterns are as follows: 1) R-N-L-[LIV]-S-[VG]-[GA]-Y-[KN]-N-[IVA]; 2) Y-K-[DE]-S-T-L-I-[IM]-Q-L-[LF]-[RHC]-D-N-[LF]-T-[LS]-W-[TAN]-[SAD].~~

Please amend the paragraph starting on line 32 of page 50 as follows:

(FKH; Pfam Accession No.PF00250). SEQ ID NO:925 corresponds to a gene encoding a polypeptide comprising a forkhead domain. The forkhead domain (also known as a "winged helix") is present in a family of eukaryotic transcription factors, and is a conserved domain of about 100 amino acid residues that is involved in DNA-binding (Weigel *et al. Cell* (1990) *63*:455-456; Clark *et al. Nature* (1993) *364*:412-420). Mammalian genes that comprise a forkhead domain include those encoding: 1) transcriptional activators (*e.g.*, HNF-3-alpha, -beta, and -gamma proteins, which interact with the cis-acting regulatory regions of a number of liver genes); 2) interleukin-enhancer binding factor (ILF), which binds to purine-rich NFAT-like motifs in the HIV-1 LTR and the interleukin-2 promoter and is involved in both positive and negative regulation of important viral and cellular promoter elements; 3) transcription factor BF-1, which plays an important role in the establishment of the regional subdivision of the developing brain and in the development of the telencephalon; 4) human HTLF,

which binds to the purine-rich region in human T-cell leukemia virus long terminal repeat (HTLV-I LTR); 5) transcription factors FREAC-1 (FKHL5, HFH-8), FREAC-2 (FKHL6), FREAC-3 (FKHL7, FKH-1), FREAC-4 (FKHL8), FREAC-5 (FKHL9, FKH-2, HFH-6), FREAC-6 (FKHL10, HFH-5), FREAC-7 (FKHL11), FREAC-8 (FKHL12, HFH-7), FKH-3, FKH-4, FKH-5, HFH-1 and HFH-4; 6) human AFX1 which is involved in a chromosomal translocation that causes acute leukemia; and 7) human FKHR which is involved in a chromosomal translocation that causes rhabdomyosarcoma. The fork domain is highly conserved, and is detected by two consensus patterns: the first corresponding to the N-terminal section of the domain; the second corresponding to a heptapeptide located in the central section of the domain. ~~The consensus patterns are as follows: 1) [KR]-P-[PTQ]-[FYLVQH]-S-[FY]-x(2)-[LIVM]-x(3,4)-[AC]-[LIM]; and 2) W-[QKR]-[NS]-S-[LIV]-R-H.~~

Please amend the paragraph starting on line 19 of page 51 as follows:

Helicases conserved C-terminal domain (helicase_C; Pfam Accession No. PF00271). SEQ ID NOS:227 and 1058 represent polynucleotides encoding novel members of the DEAD/H helicase family. The DEAD box family comprises a number of eukaryotic and prokaryotic proteins involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman, Nature (1988) 333:22 and Nature (1988) 333:578; http://www.expasy.ch/www/linder/ HELICASES_TEXT.html). One of these motifs, called the 'D-E-A-D-box', represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be 'D-E-A-H-box' proteins (Wassarman D.A., et al., Nature (1991) 349:463; Harosh I., et al., Nucleic Acids Res. (1991) 19:6331; Koonin E.V., et al., J. Gen. Virol. (1992) 73:989; http://www.expasy.ch/www/linder/ HELICASES_TEXT.html). ~~The following signature patterns are used to identify member for both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].~~

Please amend the paragraph starting on line 34 of page 51 as follows:

Kazal serine protease inhibitors family signature (Kazal; Pfam Accession No. PF00050). SEQ ID NO:97 corresponds to a polynucleotide of a gene encoding a serine protease inhibitor of the Kazal inhibitor family (Laskowski *et al. Annu. Rev. Biochem.* (1980) *49*:593-626). The basic structure of Kazal serine protease inhibitors such a type of inhibitor is described at Pfam Accession No. PF00050. Exemplary proteins known to belong to this family include: pancreatic secretory trypsin inhibitor (PSTI), whose physiological function is to prevent the trypsin-catalyzed premature activation of zymogens within the pancreas; mammalian seminal acrosin inhibitors; canidae and felidae submandibular gland double-headed protease inhibitors, which contain two Kazal-type domains, the first one inhibits trypsin and the second one elastase; a mouse prostatic secretory glycoprotein, induced by androgens, and which exhibits anti-trypsin activity; avian ovomucoids; chicken ovoinhibitor; and the leech trypsin inhibitor Bdellin B-3. ~~**The consensus pattern is as follows: C-x(7)-C-x(6)-Y-x(3)-C-x(2,3)-C, where the four C's are involved in disulfide bonds.**~~

Please amend the paragraph starting on line 22 of page 52 as follows:

Neurotransmitter-Gated Ion-Channel (neur_chan; Pfam Accession No. PF00065). SEQ ID NO:1078 corresponds to a sequence encoding a neurotransmitter-gated ion channel. Neurotransmitter-gated ion-channels, which provide the molecular basis for rapid signal transmission at chemical synapses, are post-synaptic oligomeric transmembrane complexes that transiently form a ionic channel upon the binding of a specific neurotransmitter. Five types of neurotransmitter-gated receptors are known: 1) nicotinic acetylcholine receptor (AchR); 2) glycine receptor; 3) gamma-aminobutyric-acid (GABA) receptor; 4) serotonin 5HT3 receptor; and 5) glutamate receptor. All known sequences of subunits from neurotransmitter-gated ion-channels are structurally related, and are composed of a large extracellular glycosylated N-terminal ligand-binding domain, followed by three hydrophobic transmembrane regions that form the ionic channel, followed by an intracellular region of variable length. A fourth hydrophobic region is found at the C-terminal of the sequence. ~~**The consensus pattern is: C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C, where the two C's are linked by a disulfide bond.**~~

Please amend the paragraph starting on line 18 of page 53 as follows

Protein phosphatase 2A regulatory subunit PR55 signatures (PR55; Pfam Accession No. PF01240). SEQ ID NO:1028 corresponds to a gene encoding a protine phosphatase 2A reguatory subunit. Protein phosphatase 2A (PP2A) is a serine/threonine phosphatase involved in many aspects of cellular function including the regulation of metabolic enzymes and proteins involved in signal transduction. PP2A is a trimeric enzyme that consists of a core composed of a catalytic subunit associated with a 65 Kd regulatory subunit (PR65), also called subunit A; this complex then associates with a third variable subunit (subunit B), which confers distinct properties to the holoenzyme (Mayer *et al. Trends Cell Biol.* (1994) *4*:287-291). One of the forms of the variable subunit is a 55 Kd protein (PR55) which is highly conserved in mammals (where three isoforms are known to exist). This subunit may perform a substrate recognition function or be responsible for targeting the enzyme complex to the appropriate subcellular compartment. ~~Two perfectly conserved sequences of 15 residues, one located the N-terminal region, the other in the center of the protein, serve as the basis for the consensus patterns: 1) E-F-D-Y-L-K-S-L-E-I-E-E-K-I-N; 2) N-[AG]-H-[TA]-Y-H-I-N-S-I-S-[LIVM]-N-S-D~~

Please amend the paragraph starting on line 9 of page 54 as follows:

The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in (Hanks, *et al.*, *FASEB J.* (1995) *9*:576) and covers the entire catalytic domain. ~~The consensus patterns are as follows: 1) [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP; 2) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue; and 3) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue.~~

Please amend the paragraph starting on line 17 of page 54 as follows:

Ras family proteins (ras; Pfam Accession No. PF00071). SEQ ID NO:527 represents polynucleotides encoding the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, Biochemistry 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase

activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg2+ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, Biochemistry 30:4637-4648. ~~A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.~~

Please amend the paragraph starting on line 12 of page 56 as follows:

Zinc Finger, C2H2 Type (Zincfing_C2H2; Pfam Accession No. PF00096). Several sequences corresponded to polynucleotides encoding members of the C2H2 type zinc finger protein family, which contain zinc finger domains that facilitate nucleic acid binding (Klug *et al.*, *Trends Biochem. Sci.* (1987) *12*:464; Evans *et al.*, *Cell* (1988) *52*:1; Payre *et al.*, *FEBS Lett.* (1988) *234*:245; Miller *et al.*, *EMBO J.* (1985) *4*:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) *85*:99). In addition to the conserved zinc ligand residues, a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al.*, *J. Biomol. Struct. Dyn.* (1993) *11*:557) The best conserved position, which is generally an aromatic or aliphatic residue, is located four residues after the second cysteine. ~~The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.~~

Please amend the paragraph starting on line 23 of page 56 as follows:

Zinc finger, C3HC4 type (RING finger), signature (Zincfing_C3H4; Pfam Accession No. PF00097). SEQ ID NOS:805 and 1078 represent polynucleotides encoding a polypeptide having a C3HC4 type zinc finger signature. A number of eukaryotic and viral proteins contain this signature, which is primarily a conserved cysteine-rich domain of 40 to 60 residues (Borden K.L.B., et al., *Curr. Opin. Struct. Biol.* (1996) *6*:395) that binds two atoms of zinc, and is probably involved in mediating protein-protein interactions. The 3D structure of the zinc ligation system is unique to the RING domain and is referred to as the "cross-brace" motif. ~~The spacing of the cysteines in such a domain is C-x(2)-C-x(9 to 39)-C-x(1 to 3)-H-x(2 to 3)-C-x(2)-C-x(4 to 48)-C-x(2)-C. The signature pattern for the~~

~~C3HC4 finger is based on the central region of the domain: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].~~

Please amend the paragraph starting on line 33 of page 56 as follows:

Zinc finger, CCHC type (Zincfing_CCHC; Pfam Accession No. PF00098). SEQ ID NOS:693,973, and 1078 correspond to genes encoding a member of the family of CCHC zinc fingers. Because the prototype CCHC type zinc finger structure is from an HIV protein, this domain is also referred to as a retrovrial-type zinc finger domain. The family also contains proteins involved in eukaryotic gene regulation, such as C. elegans GLH-1. The structure is an 18-residue zinc finger; no examples of indels in the alignment. ~~The motif that defines a CCHC type zinc finger domain is: C-X2-C-X4-H-X4-C (Summers J Cell Biochem 1991 Jan;45(1):41-8)~~. The domain is found in, for example, HIV-1 nucleocapsid protein, Moloney murine leukemia virus nucleocapsid protine NCp10 (De Rocquigny *et al. Nucleic Acids Res.* (1993) *21*:823-9), and myelin transcription factor 1 (Myt1) (Kim *et al. J. Neurosci. Res.* (1997) *50*:272-90).

Please amend the paragraph staring on line 9 of page 65 as follows:

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 21 below provides the ATCC Accession Nos. of the ES deposits, all of which were deposited on or before May 13, 1999. ~~The names of the clones contained within each of these deposits are provided in the tables numbered 22 and greater (inserted before the claims).~~

AMENDMENTS TO THE CLAIMS

Please cancel claims 13-66, 69, 72 and 75-102 and amend claims 67, 68 and 74. A complete listing of the claims, including their current status, is provided below.

1-66 (cancelled)

67. (Currently amended) An isolated polynucleotide comprising ~~at least 15~~ **at least 100** contiguous nucleotides of ~~a nucleotide sequence having at least 90% sequence identity to a sequence selected from the group consisting of:~~ SEQ ID NO:635~~, a degenerate variant of SEQ ID NO:635, and a complement of SEQ ID NO:635.~~ **or complement thereof.**

68. (Currently amended) An isolated polynucleotide **comprising at least 100 contiguous nucleotides of SEQ ID NO: 635 or complement thereof** which hybridizes under stringent conditions to the polynucleotide of claim 67.

69. (cancelled)

70. (Previously presented) An isolated recombinant host cell containing the polynucleotide of claim 67.

71. (Previously presented) An isolated vector comprising the polynucleotide of claim 67.

72. (Cancelled).

73. (Previously presented) An isolated polynucleotide according to claim 67, wherein the polynucleotide is a cDNA.

74. (Currently amended) An isolated cDNA **comprising at least 100 contiguous nucleotides of SEQ ID NO:635** obtained by the process of amplification using a polynucleotide comprising at least 15

contiguous nucleotides of a nucleotide sequence of SEQ ID NO:635.

75-102 (Cancelled)

REMARKS

Formal Matters

Claims 67, 68, 70, 71 and 73-74 are pending after entry of the amendments set forth herein.

Claims 13-66, 69, 72 and 75-102 are cancelled without prejudice with renewal, without intent to acquiesce to any rejection that may be applied thereon, and without the intent to abandon any subject matter encompassed therein.

Claims 67, 68 and 74 are amended. The amendments to the claims were made solely in the interest of expediting prosecution, and are not to be construed as an acquiescence to any objection or rejection of any claim. Support for the amendments to the claims is found in the claims as originally filed, and throughout the specification, in particular at the following exemplary locations: page 4 line 34 to page 5 line 2. Accordingly, no new matter is added.

Sequence Rule Compliance

The Office Action states that the application contains sequence disclosures, and, as such, a revised sequence listing is required.

To address this rejection, the Applicants have amended the specification to delete the sequences in question. The sequences are not required to support the patentability of the instant claims.

Mark Spencer at the USPTO was consulted for interpretation of the rules with respect to consensus sequences. Mr. Spencer stated that, according to the rules, only sequences with four or more invariant amino acids are required to be listed in a sequence listing. As such, the Applicants have deleted only sequences having four or more invariant amino acids.

In view of the foregoing, the Applicants submit that they complied with the requirements of 37 C.F.R § 1.821-1.825.

Biological Deposits

Claim 72 is cancelled. As such, there are no claims currently under examination that require a biological deposit.

Accordingly, the Office's objection that the conditions for deposit do not satisfy the requirement of 37 CFR § 1.808 is rendered moot.

Specification

The specification is objected to as referring to table nos. 22 and greater.

The specification has been amended to remove this reference.

In view of the foregoing, withdrawal of this rejection is respectfully requested.

Rejection of claims under 35 U.S.C. § 101/112 (Utility)

Claims 67 - 74 are rejected under 35 U.S.C. § 101/112, as lacking patentable utility.

In making this rejection, the Office states that "The claimed nucleic acids are not supported by a specific asserted utility because none of the disclosed uses of the nucleic acids in the specification is specific" and "Applicants list a number of possible uses but fail to assert a specific utility for the claimed nucleic acids". On the basis of these comments, the Office asserts that the claimed subject matter lacks specific, as opposed to a substantial or credible, utility.

The Applicants respectfully disagree.

The claimed polynucleotides find specific use in cancer diagnostics. This is a specific utility and is asserted in the instant specification in the section entitled "Diagnosis, Prognosis and Management of Cancer" starting on line 11 of page 36. In particular, the claimed polynucleotides may be used in the detection of lung, breast, prostate or colon cancer, as set forth in the detailed discussion of pages 37-39.

As such, contrary to the statements made by the Office in establishing this rejection, there *are* specific uses for the claimed polynucleotides set forth in the instant specification, and the Applicants *have* asserted a specific utility for the claimed nucleic acids.

No more is required to satisfy the utility requirement of 35 U.S.C. § 101, and, accordingly, this rejection may be withdrawn.

Rejection of claims under 35 U.S.C. § 112 (Utility)

The Applicants respectfully submit that this rejection has been addressed in the preceding section. In other words, since the claimed invention has a utility in cancer diagnostics, a skilled person would know how to use the claimed invention.

In view of the foregoing discussion, the Applicants respectfully request withdrawal of this rejection.

Rejection of claims under 35 U.S.C. § 112 (Written Description)

Claims 67-71 and 73-74 are rejected as failing to comply with the written requirement of 35 U.S.C. § 112.

Without wishing to acquiesce to the rejection, claim 67 has been amended to recite "An isolated polynucleotide comprising at least 100 contiguous nucleotides of SEQ ID NO:635 or complement thereof" and claims 68 and 74 have been amended to recite "comprising at least 100 contiguous nucleotides of SEQ ID NO:635".

The Applicants respectfully submit that the claims meet the written description requirement of 35 U.S.C. § 112 since it recites a feature that is common to all polynucleotides encompassed by the claim: 100 contiguous nucleotides of SEQ ID NO:635 or complement thereof.

The Office notes that the use of the word "comprising" in the claim causes the claim to read on full length ORFs that have yet to be discovered, and, since the full-length ORF is not specifically disclosed in the specification, reasons that claim does not meet the written description requirement of 35 U.S.C. § 112.

While the Applicants don't dispute that the claim may read on a full length ORF, the fact that a claim may read on a species that is not specifically described in the claim is not a barrier to patentability of the claim. It is well established that even in an "unpredictable art," applicants "are *not* required to disclose *every* species encompassed by their claims . . . ."[1] Thus, features that apply to only some species within a generic claim – but not to *all* species encompassed by the claim – need not be described to satisfy the written description requirement. Otherwise, to claim a genus, every species within a genus would have to be explicitly described. That is not the law.[2]

In other words, the Applicants agree with the Office in that the claimed polynucleotides read on polynucleotides that are not specifically described in the instant specification. However, as discussed in the previous paragraph, the law does not require specific disclosure of *every* species encompassed by a claim for the claim to be patentable.

Further, since the instant claims are free of the art, the Applicants respectfully submit that the "full-length ORF" to which the Office refers would be later found species encompassed by the instant

1 *In re Angstadt*, 537 F.2d 498, 502-03, 190 U.S.P.Q. (BNA) 214, 218, (C.C.P.A. 1976).
2 *See Engel Indus., Inc. v. Lockformer Co.*, 946 F.2d 1528, 1531, 20 U.S.P.Q.2d (BNA) 1300, 1302 (Fed. Cir. 1991) ("Unclaimed subject matter is not subject to the disclosure requirements of § 112; the reasons are pragmatic: the disclosure would be boundless, and the pitfalls endless."). *See also Phillips Petroleum v. U.S. Steel Corp.*, 673 F. Supp. 1278, 1292, 6 U.S.P.Q.2d (BNA) 1065, 1074 (D. Del. 1987) ("The applicant is not required to include in his application support for matters not set forth in the claim."), *aff'd* 865 F.2d 1247, 9 U.S.P.Q.2d (BNA) 1461 (Fed. Cir. 1989).

claims. Since it is well established that an explicit description of later-discovered species that now fall within a claimed genus is not required,[3] the Office's reasoning for rejecting these claims appears to be inadequate, according to the current law of written description.

In view of the foregoing, the Applicants respectfully submit that this rejection of the claims should be withdrawn without any further discussion.

Rejection of claims under 35 U.S.C. § 112 (enablement)

Claim 72 is rejected as failing to comply with the enablement requirement of 35 U.S.C. § 112, first paragraph.

Claim 72 is cancelled, and, accordingly, this rejection is moot. Withdrawal of this rejection is respectfully requested.

Rejection of claims under 35 U.S.C. § 112, second paragraph

The claims are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for reciting terms that are unclear to the Examiner.

Without wishing to acquiesce to the rejection, claim 67 has been amended to recite "An isolated polynucleotide comprising at least 100 contiguous nucleotides of SEQ ID NO:635 or complement thereof" and claims 68 and 74 have been amended to recite "comprising at least 100 contiguous nucleotides of SEQ ID NO:635".

The Applicants respectfully submit that the metes an bounds of the instant claims are clear, and, accordingly, this rejection may be withdrawn.

Rejections of claims under 35 U.S.C. § 102

The claims are rejected under 35 U.S.C. § 102(b) as anticipated by Hiller.

Hillier discloses a cDNA that has 89 contiguous nucleotides of SEQ ID NO:635.

Without wishing to acquiesce to the rejection, claim 67 has been amended to recite "An isolated polynucleotide comprising at least 100 contiguous nucleotides of SEQ ID NO:635 or complement

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3 *Rexnord Corporation v. Laitram Corporation*, 274 F.3d 1336, 1344, 60 U.S.P.Q.2d (BNA) 1851, 1856 (Fed. Cir. 2001) ("Our case law is clear that an applicant is not required to describe in the specification every conceivable and possible future embodiment of his invention."). *See also In re Hogan and Banks*, 559 F.2d 595, 605-06, 194 U.S.P.Q. (BNA) 527, 537 (C.C.P.A. 1977); *United States Steel Corporation v. Phillips Petroleum Company*, 865 F.2d 1247, 1251-52, 9 U.S.P.Q.2d (BNA) 1461, 1465 (Fed. Cir. 1989).

thereof" and claims 68 and 74 have been amended to recite "comprising at least 100 contiguous nucleotides of SEQ ID NO:635".

Since Hillier recites a cDNA that has 89 contiguous nucleotides of SEQ ID NO:635, Hillier does not disclose a polynucleotide having at least *100* contiguous nucleotides of SEQ ID NO:635. Accordingly, the claimed polynucleotides cannot be disclosed by Hillier and this rejection may be withdrawn.

The claims are rejected under 35 U.S.C. § 102(b) as anticipated by Lin.

Lin discloses a cDNA that has 17 contiguous nucleotides of SEQ ID NO:635.

Without wishing to acquiesce to the rejection, claim 67 has been amended to recite "An isolated polynucleotide comprising at least 100 contiguous nucleotides of SEQ ID NO:635 or complement thereof" and claims 68 and 74 have been amended to recite "comprising at least 100 contiguous nucleotides of SEQ ID NO:635".

Since Lin recites a cDNA that has 17 contiguous nucleotides of SEQ ID NO:635, Lin does not disclose a polynucleotide having at least *100* contiguous nucleotides of SEQ ID NO:635. Accordingly, the claimed polynucleotides cannot be disclosed by Lin and this rejection may be withdrawn.

CONCLUSION

If the Examiner believes a teleconference would expedite prosecution, he is invited to telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any fees under 37 C.F.R. §§1.16 and 1.17 which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815.

Respectfully submitted,
BOZICEVIC, FIELD & FRANCIS LLP

Date: 10-16-03

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